RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/559,711 _____
Source: _____ IFWP _____
Date Processed by STIC: _____ 02/10/2007 _____

ENTERED

IFWP

```
 3 <110> APPLICANT: Croker, Ben
 4         Roberts, Andrew
 5         Metcalf, Don
 6         Alexander, Warren
 7         Hilton, Doug
 8         Nicola, Nicos
10 <120> TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS WHICH MODULATE
11        GRANULOCITE-COLONY STIMULATING FACTOR (G-CSF) DEPENDENT
12        PROCESSES BY MODULATION OF THE LEVELS OF SUPPRESSOR OF
13        CYTOKINE SIGNALING (SOCS)
15 <130> FILE REFERENCE: 19413
17 <140> CURRENT APPLICATION NUMBER: 10/559,711
18 <141> CURRENT FILING DATE: 2005-12-05
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 682
26 <212> TYPE: DNA
27 <213> ORGANISM: human
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(678)
33 <400> SEQUENCE: 1
34 atg gtc acc cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg      48
35 Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu
36 1               5                   10                  15
38 gac acc agc ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag      96
39 Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
40                 20                  25                  30
42 ctg gtg gtg aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg     144
43 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
44             35                  40                  45
46 agc gca gtg acc ggc ggc gag gcg aac ctg ctg ctc agc gcc gag ccc     192
47 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
48      50                  55                  60
50 gcc ggc acc ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc     240
51 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
52 65                  70                  75                  80
54 acg ctc agc gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag     288
55 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
56                 85                  90                  95
58 tgt gag ggg ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag     336
59 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
```

```
60            100            105            110
63 ccc gtg ccc cgc ttc gac tgc gtg ctc aag ctg gtg cac cac tac atg      384
64 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
65            115            120            125
67 ccg ccc cct gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc      432
68 Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser
69       130            135            140
71 tcc gag gtg ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc      480
72 Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro
73 145            150            155            160
75 ccc aga aga gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg      528
76 Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
77            165            170            175
79 gtg ttg agc cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc      576
80 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
81            180            185            190
83 tgt cgg aag acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc      624
84 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
85            195            200            205
87 cag ctg ccg ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg      672
88 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
89       210            215            220
91 ctt taa gggg                                                          682
92 Leu
93 225
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 225
97 <212> TYPE: PRT
98 <213> ORGANISM: human
100 <400> SEQUENCE: 2
102 Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu
103 1            5            10            15
105 Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
106            20            25            30
108 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
109       35            40            45
111 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
112       50            55            60
114 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
115 65            70            75            80
117 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
118            85            90            95
120 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
121            100            105            110
123 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
124       115            120            125
126 Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser
127       130            135            140
129 Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro
```

```
130 145                    150                   155                 160
132 Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
133                165                   170                 175
135 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
136                180                   185                 190
138 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
139           195                   200                   205
141 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
142      210                   215                   220
144 Leu
145 225
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 2187
149 <212> TYPE: DNA
150 <213> ORGANISM: murine
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
154 <222> LOCATION: (18)..(692)
156 <400> SEQUENCE: 3
157 cgctggctcc gtgcgcc atg gtc acc cac agc aag ttt ccc gcc gcc ggg       50
158                   Met Val Thr His Ser Lys Phe Pro Ala Ala Gly
159                    1               5                 10
161 atg agc cgc ccc ctg gac acc agc ctg cgc ctc aag acc ttc agc tcc      98
162 Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser
163             15                  20                  25
165 aaa agc gag tac cag ctg gtg gtg aac gcc gtg cgc aag ctg cag gag     146
166 Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu
167          30                  35                  40
169 agc gga ttc tac tgg agc gcc gtg acc ggc ggc gag gcg aac ctg ctg     194
170 Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu
171       45                  50                  55
173 ctc agc gcc gag ccc gcg ggc acc ttt ctt atc cgc gac agc tcg gac     242
174 Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp
175 60                  65                  70                  75
177 cag cgc cac ttc ttc acg ttg agc gtc aag acc cag tcg ggg acc aag     290
178 Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys
179                80                  85                  90
181 aac cta cgc atc cag tgt gag ggg ggc agc ttt tcg ctg cag agt gac     338
182 Asn Leu Arg Ile Gln Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp
183          95                  100                 105
185 ccc cga agc acg cag cca gtt ccc cgc ttc gac tgt gta ctc aag ctg     386
186 Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu
187          110                 115                 120
189 gtg cac cac tac atg ccg cct cca ggg acc ccc tcc ttt tct ttg cca     434
190 Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro
191      125                 130                 135
193 ccc acg gaa ccc tcg tcc gaa gtt ccg gag cag cca cct gcc cag gca     482
194 Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala
195 140                 145                 150                 155
```

RAW SEQUENCE LISTING   DATE: 02/10/2007
PATENT APPLICATION: US/10/559,711   TIME: 09:52:26

Input Set : A:\19413.seqlist.txt
Output Set: N:\CRF4\02102007\J559711.raw

```
197 ctc ccc ggg agt acc ccc aag aga gct tac tac atc tat tct ggg ggc       530
198 Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly
199                 160                 165                 170
201 gag aag att ccg ctg gta ctg agc cga cct ctc tcc tcc aac gtg gcc       578
202 Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala
203                 175                 180                 185
205 acc ctc cag cat ctt tgt cgg aag act gtc aac ggc cac ctg gac tcc       626
206 Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser
207         190                 195                 200
209 tat gag aaa gtg acc cag ctg cct gga ccc att cgg gag ttc ctg gat       674
210 Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp
211     205                 210                 215
213 cag tat gat gct cca ctt taaggagcaa aagggtcaga ggggggcctg             722
214 Gln Tyr Asp Ala Pro Leu
215 220                   225
217 ggtcggtcgg tcgcctctcc tccgaggcac atggcacaag cacaaaaatc cagccccaac    782
219 ggtcggtagc tcccagtgag ccaggggcag attggcttct tcctcaggcc ctccactccc    842
221 gcagagtaga gctggcagga cctggaattc gtctgagggg aggggagct gccacctgct     902
223 ttccccctc ccccagctcc agcttcttc aagtggagcc agccggcctg gctggtggg       962
225 acaatacctt tgacaagcgg actctcccct ccccttcctc cacacccct ctgcttccca    1022
227 agggaggtgg ggacacctcc aagtgttgaa cttagaactg caaggggaat cttcaaactt   1082
229 tcccgctgga acttgtttgc gctttgattt ggtttgatca agagcaggca cctggggaa    1142
231 ggatggaaga gaaaagggtg tgtgaagggt ttttatgctg gccaaagaaa taaccactcc   1202
233 cactgcccaa cctaggtgag gagtggtggc tcctggctct ggggagagtg gcaaggggtg    1262
235 acctgaagag agctatactg gtgccaggct cctctccatg gggcagctaa tgaaacctcg    1322
237 cagatccctt gcaccccaga accctccccg ttgtgaagag gcagtagcat ttagaaggga    1382
239 gacagatgag gctggtgagc tggccgcctt ttccaacacc gaagggaggc agatcaacag    1442
241 atgagccatc ttggagccca ggtttcccct ggagcagatg gagggttctg ctttgtctct    1502
243 cctatgtggg gctaggagac tcgccttaaa tgccctctgt cccagggatg gggattggca    1562
245 cacaaggagc caaacacagc caataggcag agagttgagg gattcaccca ggtggctaca    1622
247 ggccagggga agtggctgca ggggagagac ccagtcactc caggagactc ctgagttaac    1682
249 actgggaaga cattggccag tcctagtcat ctctcggtca gtaggtccga gagcttccag    1742
251 gccctgcaca gccctccttt ctcacctggg gggaggcagg aggtgatgga gaagccttcc    1802
253 catgccgctc acaggggcct cacgggaatg cagcagccat gcaattacct ggaactggtc    1862
255 ctgtgttggg gagaaacaag ttttctgaag tcaggtatgg ggctgggtgg ggcagctgtg    1922
257 tgttggggtg gcttttttct ctctgttttg aataatgttt acaatttgcc tcaatcactt   1982
259 ttataaaaat ccacctccag cccgcccctc tccccactca ggccttcgag gctgtctgaa    2042
261 gatgcttgaa aaactcaacc aaatcccagt tcaactcaga cttttgcacat atatttatat   2102
263 ttatactcag aaaagaaaca tttcagtaat ttataataaa agagcactat tttttaatga    2162
265 aaaaaaaaaa aaaaaaaaaa aaaaa                                          2187
```

267 <210> SEQ ID NO: 4
268 <211> LENGTH: 225
269 <212> TYPE: PRT
270 <213> ORGANISM: murine

272 <400> SEQUENCE: 4

```
274 Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu
275 1               5                   10                  15
277 Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
278         20                  25                  30
```

```
280 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
281     35                  40                  45
283 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
284     50                  55                  60
286 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
287 65                  70                  75                  80
290 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
291                     85                  90                  95
293 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
294             100             105             110
296 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
297         115             120             125
299 Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro Pro Thr Glu Pro Ser
300     130             135             140
302 Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala Leu Pro Gly Ser Thr
303 145             150             155             160
305 Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
306             165             170             175
308 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
309         180             185             190
311 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
312         195             200             205
314 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
315     210             215             220
317 Leu
318 225
```

VERIFICATION SUMMARY   DATE: 02/10/2007
PATENT APPLICATION: **US/10/559,711**   TIME: 09:52:27

Input Set : **A:\19413.seqlist.txt**
Output Set: **N:\CRF4\02102007\J559711.raw**